```
=> file .nash
=> s galactosidase and common codon
L1            0 FILE MEDLINE
L2            2 FILE CAPLUS
L3            0 FILE SCISEARCH
L4            0 FILE LIFESCI
L5            0 FILE BIOSIS
L6            0 FILE EMBASE

TOTAL FOR ALL FILES
L7            2 GALACTOSIDASE AND COMMON CODON

=> d ibib abs

L7   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2002:637845  CAPLUS
DOCUMENT NUMBER:          137:180783
TITLE:                    Synthetic genes with optimized codon usage for
                          recombinant protein expression in mammals
INVENTOR(S):              Seldon, Richard F.; Miller, Allan M.; Treco, Douglas
                          S.
PATENT ASSIGNEE(S):       Transkaryotic Therapies, Inc., USA
SOURCE:                   PCT Int. Appl., 115 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
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     WO 2002064799      A2   20020822       WO 2001-US42655  20011011
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
             PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
             US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                  US 1999-407605   A1 19990929
                                        US 2000-686497   A1 20001011
AB   The present invention is directed to a synthetic nucleic acid sequence
     which encodes a protein wherein at least one non-common
     codon or less-common codon is replaced by a
     common codon. The synthetic nucleic acid sequence can
     include a continuous stretch of at least 90 codons all of which are
     common codons. Synthetic genes that have codon usages
     typical of highly expressed mammalian genes are prepd. for use in manuf.
     of the proteins using mammalian cell hosts. Recombinant expression of
     human Factor VIII and B-domain-deleted-FVIII, human Factor IX, and human
     .alpha.-galactosidase, in human fibroblast cells, is described.


=> d 2 ibib abs

L7   ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         1989:434351  CAPLUS
DOCUMENT NUMBER:          111:34351
TITLE:                    Codon usage determines translation rate in Escherichia
                          coli
AUTHOR(S):                Soerensen, Michael A.; Kurland, C. G.; Pedersen, Steen
CORPORATE SOURCE:         Inst. Microbiol., Univ. Copenhagen, Copenhagen,
                          DK-1353, Den.
SOURCE:                   Journal of Molecular Biology (1989), 207(2), 365-77
                          CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   To det. whether differences in translation rate are correlated with
```

differences in codon usage or with differences in mRNA secondary structure, a small DNA fragment was inserted in the lacZ gene either directly or flanked by a few frame-shifting bases, leaving the reading frame of the lacZ gene unchanged. The fragment was chosen to have infrequent codons in 1 reading frame and **common codons** in the other. The insert in these constructs does not seem to give mRNAs that are able to form extensive secondary structures. The translation time for these modified lacZ mRNAs was measured with a reproducibility better than plus or minus 1 s. The mRNA with infrequent codons inserted has an .apprxeq.3-s longer translation time than the 1 with **common codons**. In another set of expts. 2 almost identical lacZ genes were constructed in which the lacZ mRNAs have the potential to generate stem structures with stabilities of .apprxeq.-75 kcal/mol. In this way it was possible to investigate the influence of mRNA structure on translation rate. This type of modified gene was generated in 2 reading frames with either common or infrequent codons similar to our 1st expts. The yield of protein from these mRNAs is reduced, probably due to the action in vivo of an RNase. Nevertheless, the data do not indicate that there is any effect of mRNA secondary structure on translation rate. In contrast, the data show that there is a difference in translation rate between infrequent codons and **common codons** that is of the order of 6-fold.

```
=> s common codon
TOTAL FOR ALL FILES
L14         78 COMMON CODON

=> s l14 and human
TOTAL FOR ALL FILES
L21         16 L14 AND HUMAN

=> dup rem l21
PROCESSING COMPLETED FOR L21
L22          8 DUP REM L21 (8 DUPLICATES REMOVED)

=> d ibib abs

L22  ANSWER 1 OF 8  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:        2002:637845  CAPLUS
DOCUMENT NUMBER:         137:180783
TITLE:                   Synthetic genes with optimized codon usage for
                         recombinant protein expression in mammals
INVENTOR(S):             Seldon, Richard F.; Miller, Allan M.; Treco, Douglas
                         S.
PATENT ASSIGNEE(S):      Transkaryotic Therapies, Inc., USA
SOURCE:                  PCT Int. Appl., 115 pp.
                         CODEN: PIXXD2
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  1
PATENT INFORMATION:

     PATENT NO.       KIND  DATE           APPLICATION NO.  DATE
     ---------------  ----  --------       ---------------  --------
     WO 2002064799     A2   20020822       WO 2001-US42655  20011011
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
             PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
             US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                  US 1999-407605   A1 19990929
                                        US 2000-686497   A1 20001011
AB   The present invention is directed to a synthetic nucleic acid sequence
     which encodes a protein wherein at least one non-common
     codon or less-common codon is replaced by a
     common codon. The synthetic nucleic acid sequence can
```

include a continuous stretch of at least 90 codons all of which are **common codons**. Synthetic genes that have codon usages typical of highly expressed mammalian genes are prepd. for use in manuf. of the proteins using mammalian cell hosts. Recombinant expression of **human** Factor VIII and B-domain-deleted-FVIII, **human** Factor IX, and **human** .alpha.-galactosidase, in **human** fibroblast cells, is described.

```
=> s galactosidase and common codon
L1            0 FILE MEDLINE
L2            2 FILE CAPLUS
L3            0 FILE SCISEARCH
L4            0 FILE LIFESCI
L5            0 FILE BIOSIS
L6            0 FILE EMBASE

TOTAL FOR ALL FILES
L7            2 GALACTOSIDASE AND COMMON CODON

=> d ibib abs

L7   ANSWER 1 OF 2  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2002:637845  CAPLUS
DOCUMENT NUMBER:          137:180783
TITLE:                    Synthetic genes with optimized codon usage for
                          recombinant protein expression in mammals
INVENTOR(S):              Seldon, Richard F.; Miller, Allan M.; Treco, Douglas
                          S.
PATENT ASSIGNEE(S):       Transkaryotic Therapies, Inc., USA
SOURCE:                   PCT Int. Appl., 115 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     --------------    ----  --------       ---------------  --------
     WO 2002064799      A2   20020822       WO 2001-US42655  20011011
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
             PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
             US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                   US 1999-407605   A1 19990929
                                         US 2000-686497   A1 20001011
```

AB The present invention is directed to a synthetic nucleic acid sequence which encodes a protein wherein at least one non-**common codon** or less-**common codon** is replaced by a **common codon**. The synthetic nucleic acid sequence can include a continuous stretch of at least 90 codons all of which are **common codons**. Synthetic genes that have codon usages typical of highly expressed mammalian genes are prepd. for use in manuf. of the proteins using mammalian cell hosts. Recombinant expression of human Factor VIII and B-domain-deleted-FVIII, human Factor IX, and human .alpha.-**galactosidase**, in human fibroblast cells, is described.

```
=> d 2 ibib abs

L7   ANSWER 2 OF 2  CAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         1989:434351  CAPLUS
DOCUMENT NUMBER:          111:34351
TITLE:                    Codon usage determines translation rate in Escherichia
                          coli
AUTHOR(S):                Soerensen, Michael A.; Kurland, C. G.; Pedersen, Steen
CORPORATE SOURCE:         Inst. Microbiol., Univ. Copenhagen, Copenhagen,
                          DK-1353, Den.
```

SOURCE: Journal of Molecular Biology (1989), 207(2), 365-77
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To det. whether differences in translation rate are correlated with differences in codon usage or with differences in mRNA secondary structure, a small DNA fragment was inserted in the lacZ gene either directly or flanked by a few frame-shifting bases, leaving the reading frame of the lacZ gene unchanged. The fragment was chosen to have infrequent codons in 1 reading frame and **common codons** in the other. The insert in these constructs does not seem to give mRNAs that are able to form extensive secondary structures. The translation time for these modified lacZ mRNAs was measured with a reproducibility better than plus or minus 1 s. The mRNA with infrequent codons inserted has an .apprxeq.3-s longer translation time than the 1 with **common codons**. In another set of expts. 2 almost identical lacZ genes were constructed in which the lacZ mRNAs have the potential to generate stem structures with stabilities of .apprxeq.-75 kcal/mol. In this way it was possible to investigate the influence of mRNA structure on translation rate. This type of modified gene was generated in 2 reading frames with either common or infrequent codons similar to our 1st expts. The yield of protein from these mRNAs is reduced, probably due to the action in vivo of an RNase. Nevertheless, the data do not indicate that there is any effect of mRNA secondary structure on translation rate. In contrast, the data show that there is a difference in translation rate between infrequent codons and **common codons** that is of the order of 6-fold.

=> s common codon
TOTAL FOR ALL FILES
L14 78 COMMON CODON

=> s l14 and human
TOTAL FOR ALL FILES
L21 16 L14 AND HUMAN

=> dup rem l21
PROCESSING COMPLETED FOR L21
L22 8 DUP REM L21 (8 DUPLICATES REMOVED)

=> d ibib abs

L22 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:637845 CAPLUS
DOCUMENT NUMBER: 137:180783
TITLE: Synthetic genes with optimized codon usage for recombinant protein expression in mammals
INVENTOR(S): Seldon, Richard F.; Miller, Allan M.; Treco, Douglas S.
PATENT ASSIGNEE(S): Transkaryotic Therapies, Inc., USA
SOURCE: PCT Int. Appl., 115 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002064799	A2	20020822	WO 2001-US42655	20011011

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-407605 A1 19990929

US 2000-686497 A1 20001011

AB The present invention is directed to a synthetic nucleic acid sequence which encodes a protein wherein at least one non-**common codon** or less-**common codon** is replaced by a **common codon**. The synthetic nucleic acid sequence can include a continuous stretch of at least 90 codons all of which are **common codons**. Synthetic genes that have codon usages typical of highly expressed mammalian genes are prepd. for use in manuf. of the proteins using mammalian cell hosts. Recombinant expression of **human** Factor VIII and B-domain-deleted-FVIII, **human** Factor IX, and **human** .alpha.-galactosidase, in **human** fibroblast cells, is described.

=> s common codon
TOTAL FOR ALL FILES
L7 78 COMMON CODON

=> s l7 and human
TOTAL FOR ALL FILES
L14 16 L7 AND HUMAN

=> dup rem l14
PROCESSING COMPLETED FOR L14
L15 8 DUP REM L14 (8 DUPLICATES REMOVED)

=> d ibib abs

L15 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:637845 CAPLUS
DOCUMENT NUMBER: 137:180783
TITLE: Synthetic genes with optimized codon usage for recombinant protein expression in mammals
INVENTOR(S): Seldon, Richard F.; Miller, Allan M.; Treco, Douglas S.
PATENT ASSIGNEE(S): Transkaryotic Therapies, Inc., USA
SOURCE: PCT Int. Appl., 115 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002064799	A2	20020822	WO 2001-US42655	20011011

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-407605 A1 19990929
US 2000-686497 A1 20001011

AB The present invention is directed to a synthetic nucleic acid sequence which encodes a protein wherein at least one non-**common codon** or less-**common codon** is replaced by a **common codon**. The synthetic nucleic acid sequence can include a continuous stretch of at least 90 codons all of which are **common codons**. Synthetic genes that have codon usages typical of highly expressed mammalian genes are prepd. for use in manuf. of the proteins using mammalian cell hosts. Recombinant expression of **human** Factor VIII and B-domain-deleted-FVIII, **human** Factor IX, and **human** .alpha.-galactosidase, in **human** fibroblast cells, is described.

=> d ibib abs 2-8

L15 ANSWER 2 OF 8 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 1998025109 MEDLINE
DOCUMENT NUMBER: 98025109 PubMed ID: 9360634
TITLE: A nucleotide polymorphism in ERCC1 in **human** ovarian cancer cell lines and tumor tissues.
AUTHOR: Yu J J; Mu C; Lee K B; Okamoto A; Reed E L; Bostick-Bruton F; Mitchell K C; Reed E
CORPORATE SOURCE: Developmental Therapeutics Department, National Cancer Institute, Bethesda, MD 20892, USA.
SOURCE: MUTATION RESEARCH, (1997 Sep) 382 (1-2) 13-20.
Journal code: 0400763. ISSN: 0027-5107.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF001925
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971201

AB We studied the DNA sequence of the entire coding region of ERCC1 gene, in five cell lines established from **human** ovarian cancer (A2780, A2780/CP70, MCAS, OVCAR-3, SK-OV-3), 29 **human** ovarian cancer tumor tissue specimens, one **human** T-lymphocyte cell line (H9), and non-malignant **human** ovary tissue (NHO). Samples were assayed by PCR-SSCP and DNA sequence analyses. A silent mutation at codon 118 (site for restriction endonuclease MaeII) in exon 4 of the gene was detected in MCAS, OVCAR-3 and SK-OV-3 cells, and NHO. This mutation was a C-->T transition, that codes for the same amino acid: asparagine. This transition converts a **common codon** usage (AAC) to an infrequent codon usage (AAT), whereas frequency of use is reduced two-fold. This base change was associated with a detectable band shift on SSCP analysis. For the 29 ovarian cancer specimens, the same base change was observed in 15 tumor samples and was associated with the same band shift in exon 4. Cells and tumor tissue specimens that did not contain the C-->T transition, did not show the band shift in exon 4. Our data suggest that this alteration at codon 118 within the ERCC1 gene, may exist in platinum-sensitive and platinum-resistant ovarian cancer tissues.

L15 ANSWER 3 OF 8 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1998275804 EMBASE
TITLE: A nucleotide polymorphism in ERCC1 in **human** ovarian cancer cell lines and tumor tissues.
AUTHOR: Jing Jie Yu; Mu C.; Kang Bo Lee; Okamoto A.; Reed E.L.; Bostick-Bruton F.; Mitchell K.C.; Reed E.
CORPORATE SOURCE: E. Reed, Medical Ovarian Cancer Section, Devtl. Therapeutics Department, National Cancer Institute, Bethesda, MD 20892, United States. reed92@helix.nih.gov
SOURCE: Mutation Research - Mutation Research Genomics, (1997) 382/1-2 (13-20).
Refs: 29
ISSN: 1383-5726 CODEN: MMRGFK
PUBLISHER IDENT.: S 1383-5726(97)00004-6
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 010 Obstetrics and Gynecology
016 Cancer
022 Human Genetics
037 Drug Literature Index
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We studied the DNA sequence of the entire coding region of ERCC1 gene, in five cell lines established from **human** ovarian cancer (A2780, A2780/CP70, MCAS, OVCAR-3, SK-OV-3), 29 **human** ovarian cancer tumor tissue specimens, one **human** T-lymphocyte cell line (H9), and non-malignant **human** ovary tissue (NHO). Samples were assayed by PCR-SSCP and DNA sequence analyses. A silent mutation at codon 118 (site for restriction endonuclease MaeII) in exon 4 of the gene was detected in MCAS, OVCAR-3 and SK-OV-3 cells, and NHO. This mutation was a C .fwdarw. T transition, that codes for the same amino acid: asparagine. This transition converts a **common codon** usage (AAC) to

an infrequent codon usage (AAT), whereas frequency of use is reduced two-fold. This base change was associated with a detectable band shift on SSCP analysis. For the 29 ovarian cancer specimens, the same base change was observed in 15 tumor samples and was associated with the same band shift in exon 4. Cells and tumor tissue specimens that did not contain the C .fwdarw. T transition, did not show the band shift in exon 4. Our data suggest that this alteration at codon 118 within the ERCC1 gene, may exist in platinum- sensitive and platinum-resistant ovarian cancer tissues.

L15 ANSWER 4 OF 8 MEDLINE
ACCESSION NUMBER: 97179330 MEDLINE
DOCUMENT NUMBER: 97179330 PubMed ID: 9027616
TITLE: Clinical detection of lung cancer progression markers.
AUTHOR: Tockman M S
CORPORATE SOURCE: Johns Hopkins University School of Hygiene and Public Health, Department of Environmental Health Sciences, Baltimore, Maryland 21205, USA.
CONTRACT NUMBER: 1P50 CA58184-01 (NCI)
SOURCE: JOURNAL OF CELLULAR BIOCHEMISTRY. SUPPLEMENT, (1996) 25 177-84. Ref: 36
Journal code: 8207539. ISSN: 0733-1959.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970424
Last Updated on STN: 19970424
Entered Medline: 19970417

AB Lung cancer is the leading cause of cancer-related deaths in western countries. The prognosis for patients with lung cancer depends primarily on the stage of the tumor at the time of clinical diagnosis. New understanding of tumor biology has turned attention away from detection of clinical lung cancer, usually metastatic at presentation, toward recognition of genetic and protein markers which precede malignancy. Mutations of four types of genes contribute to the process of epithelial carcinogenesis by modifying control of cell growth. Examples of three of these changes have been detected in pre-malignant sputum, and validated in subsequent tumor. We have identified gene products (tumor associated and differentiation protein antigens), mutations of k-ras and p53, and microsatellite alterations as potential markers of subsequent malignancy. We consider the morphologic progression seen in archived sputum cells as the paradigm of neoplastic development in the lung. Although the NCl collaborative trials had shown that this progression is not recognized sufficiently often (sensitive) to be useful for lung cancer screening, this progression may be used to assess the timing of gene and peptide markers of carcinogenesis. Previous work has shown that at the time Johns Hopkins Lung Project sputum cells express moderately atypical metaplasia, 53% (8/15) of sputum specimens expressed **common** (**codon** 12) k-ras or (codons 273 or 281) p53 mutations. Other investigators have reported that earlier morphologic changes (metaplasia) accompany 3p and 9p losses of heterozygosity. These observations suggest that 3p and 9p loss likely precede k-ras or p53 mutations. Our preliminary data demonstrate that over-expression of a 31 kD tumor associated antigen recently purified, sequenced, and identified as heterogeneous nuclear ribonucleoprotein (hnRNP) A2 (with cross reactivity to splice variant B1), is expressed in most lung cancer cases before any morphologic abnormality. Comparison of the accuracy of this marker with sputum cytology will determine its value for early lung cancer detection. Preliminary evidence confirms this marker greatly improves the accuracy of standard sputum cytology for detection of lung carcinogenesis. Clinical intervention trials must be undertaken to determine whether modulation of hnRNP overexpression is useful as an intermediate endpoint for chemoprevention.

L15 ANSWER 5 OF 8 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 97054548 EMBASE
DOCUMENT NUMBER: 1997054548
TITLE: Clinical detection of lung cancer progression markers.
AUTHOR: Tockman M.S.

CORPORATE SOURCE: M.S. Tockman, School of Hygiene and Public Health, Johns Hopkins University, 615 N. Wolfe Street, Baltimore, MD 21205, United States
SOURCE: Journal of Cellular Biochemistry, (1996) 63/SUPPL. 25 (177-184).
Refs: 35
ISSN: 0730-2312 CODEN: JCEBD5
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 016 Cancer
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Lung cancer is the leading cause of cancer-related deaths in western countries. The prognosis for patients with lung cancer depends primarily on the stage of the tumor at the time of clinical diagnosis. New understanding of tumor biology has turned attention away from detection of clinical lung cancer, usually metastatic at presentation, toward recognition of genetic and protein markers which precede malignancy. Mutations of four types of genes contribute to the process of epithelial carcinogenesis by modifying control of cell growth. Examples of three of these changes have been detected in pre- malignant sputum, and validated in subsequent tumor. We have identified gene products (tumor associated and differentiation protein antigens), mutations of k-ras and p53, and microsatellite alterations as potential markers of subsequent malignancy. We consider the morphologic progression seen in archived sputum cells as the paradigm of neoplastic development in the lung. Although the NCI collaborative trials had shown that this progression is not recognized sufficiently often (sensitive) to be useful for lung cancer screening, this progression may be used to assess the timing of gene and peptide markers of carcinogenesis. Previous work has shown that at the time Johns Hopkins Lung Project sputum cells express moderately atypical metaplasia, 53% (8/15) of sputum specimens expressed **common** (**codon** 12) k-ras or (codons 273 or 281) p53 mutations. Other investigators have reported that earlier morphologic changes (metaplasia) accompany 3p and 9p losses of heterozygosity. These observations suggest that 3p and 9p loss likely precede k-ras or p53 mutations. Our preliminary data demonstrate that over-expression of a 31 kD tumor associated antigen recently purified, sequenced, and identified as heterogeneous nuclear ribonucleoprotein (hnRNP) A2 (with cross reactivity to splice variant B1), is expressed in most lung cancer cases before any morphologic abnormality. Comparison of the accuracy of this marker with sputum cytology will determine its value for early lung cancer detection. Preliminary evidence confirms this marker greatly improves the accuracy of standard sputum cytology for detection of lung carcinogenesis. Clinical intervention trials must be undertaken to determine whether modulation of hnRNP overexpression is useful as an intermediate endpoint for chemoprevention.

L15 ANSWER 6 OF 8 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 97083381 MEDLINE
DOCUMENT NUMBER: 97083381 PubMed ID: 8929955
TITLE: Familial adenomatous polyposis in a 5 year old child: a clinical, pathological, and molecular genetic study.
AUTHOR: Distante S; Nasioulas S; Somers G R; Cameron D J; Young M A; Forrest S M; Gardner R J
CORPORATE SOURCE: The Murdoch Institute, Royal Children's Hospital, Melbourne, Australia.
SOURCE: JOURNAL OF MEDICAL GENETICS, (1996 Feb) 33 (2) 157-60.
Journal code: 2985087R. ISSN: 0022-2593.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970523
Last Updated on STN: 19970523
Entered Medline: 19970512

AB A girl aged 5 years 8 months presented with rectal bleeding; her father had had familial adenomatous polyposis (FAP) and a colectomy at the age of 23. Endoscopy showed extensive polyposis and she had a colectomy. The proband and her father had the **common codon** 1309 5 bp

deletion APC mutation. This mutation predisposes to early onset of FAP, and consideration needs to be given to having molecular testing of at risk members of these families done in childhood.

L15 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:66454 CAPLUS
DOCUMENT NUMBER: 122:78365
TITLE: An A-to-C substitution involving the translation initiation codon in a patient with myophosphorylase deficiency (McArdle's disease)
AUTHOR(S): Tsujino, Seiichi; Rubin, Laurence A.; Shanske, Sara; DiMauro, Salvatore
CORPORATE SOURCE: H. Houston Merritt Clinical Research Center Muscular Dystrophy and related diseases, New York, NY, 10032, USA
SOURCE: Human Mutation (1994), 4(1), 73-5
CODEN: HUMUE3; ISSN: 1059-7794
DOCUMENT TYPE: Journal
LANGUAGE: English
AB RFLP screening of white blood cell genomic DNA from a 36-yr-old woman with McArdle's disease indicated that she had the relatively **common codon** 49 nonsense mutation in one allele but another mutation in her other allele. Sequencing of the other allele revealed an A-to-C substitution in the initiation codon for the myophosphorylase gene, changing it to CTG.

L15 ANSWER 8 OF 8 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 89255401 MEDLINE
DOCUMENT NUMBER: 89255401 PubMed ID: 2656695
TITLE: Expression of **human** thymidylate synthase in Escherichia coli.
COMMENT: Erratum in: J Biol Chem 1994 Dec 2;269(48):30740
AUTHOR: Davisson V J; Sirawaraporn W; Santi D V
CORPORATE SOURCE: Department of Biochemistry and Biophysics, University of California, San Francisco 94143.
CONTRACT NUMBER: 5T32CA09270 (NCI)
CA14394 (NCI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1989 Jun 5) 264 (16) 9145-8.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198907
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19980206
Entered Medline: 19890705
AB A cDNA clone encoding thymidylate synthase (TS) has been isolated from a **human** T-cell library and modified in the 5'-untranslated region to incorporate several unique cloning sites. The gene has been cloned as a cassette into several Escherichia coli expression vectors which did not provide detectable amounts of the enzyme. A successful approach used a constitutive E. coli expression vector developed for the enzyme from Lactobacillus casei. A 115-base pair 5'-untranslated region from the L. casei TS which contains a ribosomal binding site and other regulatory sequences has been fused to the coding region of the **human** TS gene to provide a construct that is expressed in E. coli. The level of expression was further enhanced by altering the nucleotide sequence of the first 90 base pairs to accommodate **common codon** use in E. coli. In our best expression system, catalytically active **human** TS is expressed to a level that represents about 1.6% of the total soluble protein. The recombinant **human** TS has been purified and characterized; except for the presence of an amino-terminal blocking group, the enzyme has physical and kinetic properties similar to the enzyme isolated from **human** cells.

=> log y

```
=> s galactosidase and fabry

TOTAL FOR ALL FILES
L7        2081 GALACTOSIDASE AND FABRY

=> s l2 and human


TOTAL FOR ALL FILES
L14       1585 L2 AND HUMAN

=> s l7 and human
TOTAL FOR ALL FILES
L21       1585 L7 AND HUMAN

=> s l21 and .alpha.
TOTAL FOR ALL FILES
L28       1491 L21 AND .ALPHA.

=> s l28 not 1990-2002/py
L29        175 FILE MEDLINE
L30         57 FILE CAPLUS
L31          4 FILE SCISEARCH
L32          3 FILE LIFESCI
L33        107 FILE BIOSIS
L34         98 FILE EMBASE

TOTAL FOR ALL FILES
L35        444 L28 NOT 1990-2002/PY

=> d 1-10 129 ibib abs
YOU HAVE REQUESTED DATA FROM FILE 'MEDLINE' - CONTINUE? (Y)/N:y



L29  ANSWER 1 OF 175     MEDLINE
ACCESSION NUMBER:   91027226     MEDLINE
DOCUMENT NUMBER:    91027226   PubMed ID: 2908672
TITLE:              Anderson-Fabry disease--family linkage studies
                    using two polymorphic X-linked DNA probes.
AUTHOR:             Morgan S H; Cheshire J K; Wilson T M; MacDermot K; Crawfurd
                    M A
CORPORATE SOURCE:   Division of Inherited Metabolic Diseases, MRC Clinical
                    Research Centre, Harrow, Middlesex, UK.
SOURCE:             PEDIATRIC NEPHROLOGY, (1987 Jul) 1 (3) 536-9.
                    Journal code: 8708728. ISSN: 0931-041X.
PUB. COUNTRY:       GERMANY: Germany, Federal Republic of
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        199012
ENTRY DATE:         Entered STN: 19910208
                    Last Updated on STN: 19950206
                    Entered Medline: 19901227
AB   Anderson-Fabry disease is an X-linked lysosomal storage disorder
     due to alpha-galactosidase A deficiency. In affected
     males there is a high mortality in early adult life due to renal failure
     and cardiovascular complications. We describe our preliminary results from
     genetic linkage studies in five families using two polymorphic DNA probes,
     DXS17 and DXYS1, mapping to an area on the long arm of the X chromosome
     between Xql3-22. DXS17 identified a Taql polymorphism closely linked to
     the disease locus in three families (lodmax Z = 4.23. at a recombination
     fraction decreases theta = 0.0). Restriction fragment length polymorphisms
     detected by DXYS1 were not linked.

L29  ANSWER 2 OF 175     MEDLINE
ACCESSION NUMBER:   90299318     MEDLINE
DOCUMENT NUMBER:    90299318   PubMed ID: 2561653
TITLE:              [Fabry's disease: kidney insufficiency in
                    heterozygous patient].
                    Malattia di Fabry: insufficienza renale in
```

eterozigote.
AUTHOR: Pravata G; Pinto G; Noto G; Arico M
SOURCE: GIORNALE ITALIANO DI DERMATOLOGIA E VENEREOLOGIA, (1989 Nov-Dec) 124 (11-12) 505-9.
Journal code: 8102852. ISSN: 0026-4741.
PUB. COUNTRY: Italy
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Italian
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199008
ENTRY DATE: Entered STN: 19900907
Last Updated on STN: 19990129
Entered Medline: 19900806
AB We report a rare heterozygous status for **Fabry**'s gene with severe kidney involvement and normal **alpha-galactosidase** A activity, together with the intrafamilial variations in the clinical expression of the disease. The random X inactivation hypothesis seems to explain such a variable expression of the **alpha-galactosidase** gene in our cases.

L29 ANSWER 3 OF 175 MEDLINE
ACCESSION NUMBER: 90296528 MEDLINE
DOCUMENT NUMBER: 90296528 PubMed ID: 2561643
TITLE: The gene encoding **alpha-galactosidase** A and gene rearrangements causing **Fabry** disease.
AUTHOR: Kornreich R; Bishop D F; Desnick R J
CORPORATE SOURCE: Division of Medical and Molecular Genetics, Mount Sinai School of Medicine, New York, NY 10029.
CONTRACT NUMBER: 2 T32 HD07105 (NICHD)
5 M01 RR00071 (NCRR)
5 R01 DK34045 (NIDDK)
SOURCE: TRANSACTIONS OF THE ASSOCIATION OF AMERICAN PHYSICIANS, (1989) 102 30-43.
Journal code: 7506109. ISSN: 0066-9458.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199007
ENTRY DATE: Entered STN: 19900907
Last Updated on STN: 19990129
Entered Medline: 19900727

L29 ANSWER 4 OF 175 MEDLINE
ACCESSION NUMBER: 90145947 MEDLINE
DOCUMENT NUMBER: 90145947 PubMed ID: 2559640
TITLE: [**Fabry**'s disease and Klippel-Trenaunay syndrome of the 4 limbs].
Maladie de **Fabry** et syndrome de Klippel-Trenaunay des quatre membres.
AUTHOR: Enjolras O; Leibowitch M; Riche M C; Lizop M; Escande J P
CORPORATE SOURCE: Service de Dermatologie, Hopital Tarnier, Paris.
SOURCE: ANNALES DE DERMATOLOGIE ET DE VENEREOLOGIE, (1989) 116 (11) 788-90.
Journal code: 7702013. ISSN: 0151-9638.
PUB. COUNTRY: France
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: French
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199003
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19900328
Entered Medline: 19900315

L29 ANSWER 5 OF 175 MEDLINE
ACCESSION NUMBER: 90116512 MEDLINE
DOCUMENT NUMBER: 90116512 PubMed ID: 2855953
TITLE: **Alpha-galactosidase** A deficiency--**Fabry**'s disease.
AUTHOR: Tsuji S
SOURCE: TANPAKUSHITSU KAKUSAN KOSO. PROTEIN, NUCLEIC ACID, ENZYME,

(1988 Apr) 33 (5) 745-8.
Journal code: 0413762. ISSN: 0039-9450.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Japanese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199002
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19990129
Entered Medline: 19900220

L29 ANSWER 6 OF 175 MEDLINE
ACCESSION NUMBER: 90080835 MEDLINE
DOCUMENT NUMBER: 90080835 PubMed ID: 2556612
TITLE: Detection of **Fabry**'s disease carriers by enzyme assay of hair roots.
COMMENT: Comment in: J Inherit Metab Dis. 1989;12(4):491-2
AUTHOR: Hatton C E; Cooper A; Sardharwalla I B
CORPORATE SOURCE: Willink Biochemical Genetics Unit, Royal Manchester Children's Hospital, Pendleburg, UK.
SOURCE: JOURNAL OF INHERITED METABOLIC DISEASE, (1989) 12 Suppl 2 369-71.
Journal code: 7910918. ISSN: 0141-8955.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199001
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19990129
Entered Medline: 19900125

L29 ANSWER 7 OF 175 MEDLINE
ACCESSION NUMBER: 90068337 MEDLINE
DOCUMENT NUMBER: 90068337 PubMed ID: 2555802
TITLE: Anderson **Fabry** disease--an identifiable disorder.
AUTHOR: Wakeel R; Shibib K; Chapman R; Dunnigan M
SOURCE: PRACTITIONER, (1989 Mar 8) 233 (1464) 294-5.
Journal code: 0404245. ISSN: 0032-6518.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199001
ENTRY DATE: Entered STN: 19900328
Last Updated on STN: 19990129
Entered Medline: 19900102

L29 ANSWER 8 OF 175 MEDLINE
ACCESSION NUMBER: 89360761 MEDLINE
DOCUMENT NUMBER: 89360761 PubMed ID: 2504843
TITLE: Transvenous permanent pacemaker implantation for **Fabry**'s disease. 3 cases report.
AUTHOR: Yoshida K; Murase M; Maseki T; Usui A; Ina H; Abe T
SOURCE: NIPPON KYOBU GEKA GAKKAI ZASSHI. JOURNAL OF THE JAPANESE ASSOCIATION FOR THORACIC SURGERY, (1989 Feb) 37 (2) 386-90.
Journal code: 19130180R. ISSN: 0369-4739.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Japanese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198909
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19990129
Entered Medline: 19890928
AB Three men with **Fabry**'s disease (angiokeratoma corporis diffusum universal) are described. In the first patient, atrial fibrillation appeared, and a permanent cardiac pacemaker (VVI) was implanted. Sick sinus syndrome with complete atrioventricular block was occurred on the second patient. Transvenous pacemaker (DDD) implantation was performed for him. The last patient was younger brother of the second patient. He

demonstrated complete atrio-ventricular block, so cardiac pace maker (VAT) was implanted. They showed a low value of granulocyte's **alpha-galactosidase** activity. During 1 to 4 year follow up period, they showed no trouble about pacemaking. **Fabry**'s disease is an disorder of glycosphingolipid metabolism. This disorder is characterized by the accumulation of trihexosyl ceramide in many sites. Cardiac involvement and abnormal electrocardiographic manifestations are common in this disorder. Permanent cardiac pacemaker is necessary for severe bradycardia caused by this disorder.

L29 ANSWER 9 OF 175 MEDLINE
ACCESSION NUMBER: 89355456 MEDLINE
DOCUMENT NUMBER: 89355456 PubMed ID: 2504516
TITLE: Angiokeratoma corporis diffusum in GM1 gangliosidosis, type 1.
AUTHOR: Beratis N G; Varvarigou-Frimas A; Beratis S; Sklower S L
CORPORATE SOURCE: Department of Pediatrics, University of Patras Medical School, Greece.
SOURCE: CLINICAL GENETICS, (1989 Jul) 36 (1) 59-64.
Journal code: 0253664. ISSN: 0009-9163.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198910
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 19990129
Entered Medline: 19891004
AB A patient with severe deficiency of beta-**galactosidase**, who developed skin lesions of angiokeratoma corporis diffusum between the 3rd and 10th month of life, is described. The activity of other lysosomal enzymes, including **alpha**-neuraminidase, was normal. The first signs of the disease were noticed during the first month of life. By 3 months coarseness of the face and psychomotor retardation were present. In addition to angiokeratoma, he had large mongolian spots and several scattered slate-blue spots of pigmentation over his body. With the exception of the skin lesions, the other clinical signs and the course of the psychomotor deterioration were within the clinical picture of GM1 gangliosidosis, Type 1. Angiokeratoma, a manifestation of several lysosomal disorders, may appear in GM1 gangliosidosis during the first year of life.

L29 ANSWER 10 OF 175 MEDLINE
ACCESSION NUMBER: 89323245 MEDLINE
DOCUMENT NUMBER: 89323245 PubMed ID: 2546612
TITLE: [Substrate specificity of multiple forms of **human** **alpha**-D-**galactosidase** and **alpha**-D-fucosidase].
Substratnaia spetsifichnost' mnozhestvennykh form **alpha**-D-galaktozidazy i **alpha**-D-fukozidazy cheloveka.
AUTHOR: Baskaeva E M; Shono N I; Kozlova I K; Vidershain G Ia
SOURCE: BIOKHIMIIA, (1989 Mar) 54 (3) 421-6.
Journal code: 0372667. ISSN: 0320-9725.
PUB. COUNTRY: USSR
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Russian
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198908
ENTRY DATE: Entered STN: 19900309
Last Updated on STN: 20000303
Entered Medline: 19890829
AB It was shown that **human** **alpha**-D-**galactosidase** is represented by multiple forms, only one of which can also split **alpha**-D-fucoside. **Fabry**'s disease was found to be associated not only with the deficiency of the **alpha**-D-**galactosidase** total activity but also with the deficiency of the **alpha**-D-fucosidase activity. The decrease in the **alpha**-D-**galactosidase** activity is due to the lack of two enzyme forms, while the profile of **alpha**-D-fucosidase multiple forms during isoelectric focusing of **human** enzyme preparations is

modified very little in comparison with the normal one. The deficiency of both enzymes was expressed in most degree in leukocytes as compared to other tissues. The residual activities of **alpha**-D-**galactosidase** and **alpha**-D-fucosidase in leukocytes were equal to 3.5 and 21%, respectively. Since the decrease in the **alpha**-D-fucosidase activity was not so noticeable as in the **alpha**-D-**galactosidase** activity, it may be expected that the determination of the **alpha**-D-fucosidase activity can no longer be regarded as a reliable test for the diagnosis of **Fabry** 's disease. The data obtained suggest that **alpha**-D-galactoside and **alpha**-D-fucoside are split by the same enzyme, the multiple forms of which are characterized by selective specificity towards these substrates.

WEST Search History

DATE: Monday, October 28, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L10	common codon	25	L10
L9	galactosidase and common adj1 codon	4	L9
L8	human and galactosidase and (nucleic acid or dna or cdna or rna or mrna) and common adj1 codon	4	L8
L7	human and galactosidase and (nucleic acid or dna or cdna or rna of mrna) and common adj1 codon	4	L7
DB=USPT,PGPB; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L6	human same galactosidase and (nucleic acid or dna or cdna or rna of mrna) and common adj1 codon	0	L6
L5	L4 and common codon	0	L5
L4	human same galactosidase and (nucleic acid or dna or cdna or rna of mrna)	2437	L4
L3	L2 and (nucleic acid or dna or cdna or rna of mrna)	14694	L3
L2	galactosidase	16508	L2
DB=USPT; THES=ASSIGNEE; PLUR=YES; OP=ADJ			
L1	galactosidase	13369	L1

END OF SEARCH HISTORY

WEST

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Search Results - Record(s) 1 through 4 of 4 returned.

☐ 1. Document ID: US 20020123083 A1

L9: Entry 1 of 4 File: PGPB Sep 5, 2002

PGPUB-DOCUMENT-NUMBER: 20020123083
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020123083 A1

TITLE: Nucleic acid endocing growth factor protein

PUBLICATION-DATE: September 5, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Shigeta, Ron T. JR.	Berkeley	CA	US	
Siani-Rose, Michael A.	San Francisco	CA	US	

US-CL-CURRENT: 435/7.23; 435/320.1, 435/325, 435/69.4, 530/399, 536/23.5, 702/19, 800/8

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 6232458 B1

L9: Entry 2 of 4 File: USPT May 15, 2001

US-PAT-NO: 6232458
DOCUMENT-IDENTIFIER: US 6232458 B1

TITLE: Synthetic polynucleotides encoding tropoelastin

DATE-ISSUED: May 15, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weiss; Anthony Steven	Sydney			AU
Martin; Stephen Lewis	Sedgley			GB

US-CL-CURRENT: 536/23.5; 435/252.33, 435/254.1, 435/254.2, 435/320.1, 435/69.1, 435/69.7, 530/353, 536/23.4, 536/24.1, 536/24.2

ABSTRACT:

Recombinant tropoelastins and variants of recombinant tropoelastins produced from synthetic polynucleotides, as well as the synthetic polynucleotides themselves are provided. Also provided are cross-linked elastins or elastin-like products prepared from the tropoelastins or variants.

24 Claims, 21 Drawing figures

Exemplary Claim Number: 1
Number of Drawing Sheets: 21

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw. Desc | Image

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☐ 3. Document ID: US 5955277 A

L9: Entry 3 of 4 File: USPT Sep 21, 1999

US-PAT-NO: 5955277
DOCUMENT-IDENTIFIER: US 5955277 A

TITLE: Mutant cDNA encoding the p85.alpha. subunit of phosphatidylinositol 3-kinase

DATE-ISSUED: September 21, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Hansen; Torben	Hellerup			DK
Andersen; Carsten Bo	Los Altos	CA		
Pedersen; Oluf Borbye	Holte			DK

US-CL-CURRENT: 435/6; 435/91.2, 536/23.1

ABSTRACT:

The present invention relates to a mutant cDNA sequence encoding the regulatory p85.alpha. subunit of phosphatidylinositol 3-kinase (PI3K), a method of detecting a mutation in the gene encoding the regulatory p85.alpha. subunit of phosphatidylinositol 3-kinase, as well as a diagnostic composition and a test kit for use in the method.

20 Claims, 2 Drawing figures
Exemplary Claim Number: 1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw. Desc | Image

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☐ 4. Document ID: US 5246844 A

L9: Entry 4 of 4 File: USPT Sep 21, 1993

US-PAT-NO: 5246844
DOCUMENT-IDENTIFIER: US 5246844 A

TITLE: Virulence associated proteins in Borrelia burgdorferi (BB)

DATE-ISSUED: September 21, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Norris; Steven J.	Houston	TX		
Barbour; Alan G.	San Antonio	TX		

US-CL-CURRENT: 435/480; 435/252.3, 435/252.33, 435/320.1, 435/476, 435/488, 536/23.7,

WEST

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Search Results - Record(s) 1 through 20 of 25 returned.

1. Document ID: US 20020137720 A1

L10: Entry 1 of 25 File: PGPB Sep 26, 2002

PGPUB-DOCUMENT-NUMBER: 20020137720
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020137720 A1

TITLE: Papilloma virus sequences

PUBLICATION-DATE: September 26, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ertl, Peter F.	Stevenage		GB	
Gough, Gerald W.	Stevenage		GB	
Ring, Christopher Jeffrey Alan	Stevenage		GB	
Parmar, Vanita	Stevenage		GB	
Walcott, Sarah Marina	Stevenage		GB	

US-CL-CURRENT: 514/45; 435/235.1, 435/252.3, 435/325, 435/91.1, 514/44, 536/23.72

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

2. Document ID: US 20020123083 A1

L10: Entry 2 of 25 File: PGPB Sep 5, 2002

PGPUB-DOCUMENT-NUMBER: 20020123083
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020123083 A1

TITLE: Nucleic acid endocing growth factor protein

PUBLICATION-DATE: September 5, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Shigeta, Ron T. JR.	Berkeley	CA	US	
Siani-Rose, Michael A.	San Francisco	CA	US	

US-CL-CURRENT: 435/7.23; 435/320.1, 435/325, 435/69.4, 530/399, 536/23.5, 702/19, 800/8

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

☐ 3. Document ID: US 6366860 B1

L10: Entry 3 of 25 File: USPT Apr 2, 2002

US-PAT-NO: 6366860
DOCUMENT-IDENTIFIER: US 6366860 B1

TITLE: Synthetic genes for enhanced expression

DATE-ISSUED: April 2, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Rozzell, Jr.; J. David	Burbank	CA		
Bui; Peter	El Monte	CA		

US-CL-CURRENT: 702/27; 540/456, 540/460, 702/19, 702/30, 702/32

ABSTRACT:

A method of making a synthetic nucleic acid sequence comprises providing a starting nucleic acid sequence, which optionally encodes an amino acid sequence, and determining the predicted .DELTA.G.sub.folding of the sequence. The starting nucleic acid sequence can be a naturally occurring sequence or a non-naturally occurring sequence. The starting nucleic acid sequence is modified by replacing at least one codon from the starting nucleic acid sequence with a different corresponding codon to provide a modified nucleic acid sequence. As used herein, a "different corresponding codon" refers to a codon which does not have the identical nucleotide sequence, but which encodes the identical amino acid. The predicted .DELTA.G.sub.folding of the modified nucleic acid sequence is determined and compared with the .DELTA.G.sub.folding of the starting nucleic acid sequence. In accordance with the invention, the predicted .DELTA.G.sub.folding of the starting nucleic acid sequence can be determined before or after the modified starting nucleic acid is provided.

23 Claims, 10 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 7

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 4. Document ID: US 6365390 B1

L10: Entry 4 of 25 File: USPT Apr 2, 2002

US-PAT-NO: 6365390
DOCUMENT-IDENTIFIER: US 6365390 B1

TITLE: Phenolic acid esterases, coding sequences and methods

DATE-ISSUED: April 2, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Blum; David L.	San Diego	CA		
Kataeva; Irina	Athens	GA		
Li; Xin-Liang	Athens	GA		
Ljungdahl; Lars G.	Athens	GA		

US-CL-CURRENT: 435/197; 435/183, 435/252.3, 435/320.1, 530/350, 536/23.1, 536/23.2

ABSTRACT:

Described herein are four phenolic acid esterases, three of which correspond to domains of previously unknown function within bacterial xylanases, from XynY and XynZ of Clostridium thermocellum and from a xylanase of Ruminococcus. The fourth specifically exemplified xylanase is a protein encoded within the genome of Orpinomyces PC-2. The amino acids of these polypeptides and nucleotide sequences encoding them are provided. Recombinant host cells, expression vectors and methods for the recombinant production of phenolic acid esterases are also provided.

26 Claims, 13 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 11

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 5. Document ID: US 6337181 B1

L10: Entry 5 of 25 File: USPT Jan 8, 2002

US-PAT-NO: 6337181
DOCUMENT-IDENTIFIER: US 6337181 B1

TITLE: Method of specifying vaccine components for viral quasispecies

DATE-ISSUED: January 8, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Stewart; Jeffrey Joseph	Chatham	NJ	07928	
Litwin; Samuel	Elkins Pk.	PA	19027	
Watts; Perry	Elkins Pk.	PA	19027	

US-CL-CURRENT: 435/5; 424/184.1, 424/206.1, 424/93.21, 435/320.1, 435/325, 435/455, 514/44, 530/351

ABSTRACT:

An algorithm for determining the viral antigenic protein variants to be used to construct vaccines designed to immunize against variable viral populations (quasispecies) is described. The method entails analyzing multiple nucleotide sequences of viral proteins and identifying those variants that provide selective advantage to the virus. Examples are given for influenza A hemagglutinin 3 and HIV-1 gp120.

16 Claims, 2 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 6. Document ID: US 6333172 B1

L10: Entry 6 of 25 File: USPT Dec 25, 2001

US-PAT-NO: 6333172
DOCUMENT-IDENTIFIER: US 6333172 B1

TITLE: Genes and proteins controlling cholesterol synthesis

DATE-ISSUED: December 25, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Rine; Jasper D.	Moraga	CA		
Hampton; Randolph	San Diego	CA		

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/455

ABSTRACT:

The present invention provides isolated nucleic acid sequences which encode a family of HMG-CoA Reductase Degradation (HRD) polypeptides. More particularly, the present invention provides isolated HRD1, HRD2 and HRD3 nucleic acids and the Hrd polypeptides encoded by such nucleic acids, i.e., Hrd1, Hrd2 and Hrd3, respectively. Vectors comprising the nucleic acids are provided. In addition, the present invention provides screening assay related to cholesterol biosynthesis.

36 Claims, 11 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 10

7. Document ID: US 6232458 B1

L10: Entry 7 of 25 File: USPT May 15, 2001

US-PAT-NO: 6232458
DOCUMENT-IDENTIFIER: US 6232458 B1

TITLE: Synthetic polynucleotides encoding tropoelastin

DATE-ISSUED: May 15, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Weiss; Anthony Steven	Sydney			AU
Martin; Stephen Lewis	Sedgley			GB

US-CL-CURRENT: 536/23.5; 435/252.33, 435/254.1, 435/254.2, 435/320.1, 435/69.1, 435/69.7, 530/353, 536/23.4, 536/24.1, 536/24.2

ABSTRACT:

Recombinant tropoelastins and variants of recombinant tropoelastins produced from synthetic polynucleotides, as well as the synthetic polynucleotides themselves are provided. Also provided are cross-linked elastins or elastin-like products prepared from the tropoelastins or variants.

24 Claims, 21 Drawing figures
Exemplary Claim Number: 1

Number of Drawing Sheets: 21

☐ 8. Document ID: US 6184018 B1

L10: Entry 8 of 25 File: USPT Feb 6, 2001

US-PAT-NO: 6184018
DOCUMENT-IDENTIFIER: US 6184018 B1

TITLE: .beta.-glucosidase coding sequences and protein from orpinomyces PC-2

DATE-ISSUED: February 6, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Li; Xin-Liang	Athens	GA		
Ljungdahl; Lars G.	Athens	GA		
Chen; Huizhong	Lawrenceville	GA		
Ximenes; Eduardo A.	Athens	GA		

US-CL-CURRENT: 435/209; 435/183, 435/252.3, 435/252.31, 435/252.35, 435/254.11, 435/254.21, 435/254.23, 435/254.5, 435/254.6, 435/255.5, 435/320.1, 435/69.1, 536/23.1, 536/23.2

ABSTRACT:

Provided is a novel .beta.-glucosidase from Orpinomyces sp. PC2, nucleotide sequences encoding the mature protein and the precursor protein, and methods for recombinant production of this .beta.-glucosidase.

13 Claims, 7 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 5

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 9. Document ID: US 6114158 A

L10: Entry 9 of 25 File: USPT Sep 5, 2000

US-PAT-NO: 6114158
DOCUMENT-IDENTIFIER: US 6114158 A

TITLE: Orpinomyces cellulase celf protein and coding sequences

DATE-ISSUED: September 5, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Li; Xin-Liang	Athens	GA		
Chen; Huizhong	Athens	GA		
Ljungdahl; Lars G.	Athens	GA		

US-CL-CURRENT: 435/209; 435/252.3, 536/23.2

ABSTRACT:

A cDNA (1,520 bp), designated celF, consisting of an open reading frame (ORF) encoding a polypeptide (CelF) of 432 amino acids was isolated from a cDNA library of the anaerobic rumen fungus Orpinomyces PC-2 constructed in Escherichia coli. Analysis of the deduced amino acid sequence showed that starting from the N-terminus, CelF consists of a signal peptide, a cellulose binding domain (CBD) followed by an extremely Asn-rich linker region which separate the CBD and the catalytic domains. The latter is located at the C-terminus. The catalytic domain of CelF is highly homologous to CelA and CelC of Orpinomyces PC-2, to CelA of Neocallimastix patriciarum and also to cellobiohydrolase IIs (CBHIIs) from aerobic fungi. However, Like CelA of Neocallimastix patriciarum, CelF does not have the noncatalytic repeated peptide domain (NCRPD) found in CelA and CelC from the same organism. The recombinant protein CelF hydrolyzes cellooligosaccharides in the pattern of CBHII, yielding only cellobiose as product with cellotetraose as the substrate. The genomic celF is interrupted by a 111 bp intron, located within the region coding for the CBD. The intron of the celF has features in common with genes from aerobic filamentous fungi.

20 Claims, 3 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 4

☐ 10. Document ID: US 6110720 A

L10: Entry 10 of 25 File: USPT Aug 29, 2000

US-PAT-NO: 6110720
DOCUMENT-IDENTIFIER: US 6110720 A

TITLE: Orpinomyces cellulase CelE protein and coding sequences

DATE-ISSUED: August 29, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Li; Xin-Liang	Athens	GA		
Ljungdahl; Lars G.	Athens	GA		
Chen; Huizhong	Athens	GA		

US-CL-CURRENT: 435/209; 435/252.3, 435/252.33, 536/23.2

ABSTRACT:

A CDNA designated celE cloned from Orpinomyces PC-2 encodes a polypeptide (CelE) of 477 amino acids. CelE is highly homologous to CelB of Orpinomyces (72.3% identity) and Neocallimastix (67.9% identity), and like them, it has a non-catalytic repeated peptide domain (NCRPD) at the C-terminal end. The catalytic domain of CelE is homologous to glycosyl hydrolases of Family 5, found in several anaerobic bacteria. The gene of celE is devoid of introns. The recombinant proteins CelE and CelB of Orpinomyces PC-2 randomly hydrolyze carboxymethylcellulose and cello-oligosaccharides in the pattern of

endoglucanases.

9 Claims, 2 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 2

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

☐ 11. Document ID: US 6107462 A

L10: Entry 11 of 25 File: USPT Aug 22, 2000

US-PAT-NO: 6107462
DOCUMENT-IDENTIFIER: US 6107462 A

TITLE: Genes and proteins controlling cholesterol synthesis

DATE-ISSUED: August 22, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Rine; Jasper D.	Moraga	CA		
Hampton; Randolph	San Diego	CA		

US-CL-CURRENT: 530/350; 435/69.1, 536/23.5, 536/23.7

ABSTRACT:

The present invention provides isolated nucleic acid sequences which encode a family of HMG-CoA Reductase Degradation (HRD) polypeptides. More particularly, the present invention provides isolated HRD1, HRD2 and HRD3 nucleic acids and the Hrd polypeptides encoded by such nucleic acids, i.e., Hrd1, Hrd2 and Hrd3, respectively. Vectors comprising the nucleic acids are provided. In addition, the present invention provides screening assay related to cholesterol biosynthesis.

5 Claims, 10 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 10

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

☐ 12. Document ID: US 5989903 A

L10: Entry 12 of 25 File: USPT Nov 23, 1999

US-PAT-NO: 5989903
DOCUMENT-IDENTIFIER: US 5989903 A

TITLE: Strain for the production of 6-dimethyltetracycline, method for producing the strain and vector for use in the method

DATE-ISSUED: November 23, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ryan; Michael J.	West Milford	NJ		

US-CL-CURRENT: 435/320.1; 435/183, 435/252.3, 435/252.35, 435/471, 435/64, 536/23.2, 536/23.7, 536/24.1

ABSTRACT:

Recombinant S. aureofaciens cells are provided. These cells comprise:

(a) at least one CTC 11 gene; and (b) optionally

(i) a CTC 09 gene;

(ii) a CTC 03 gene; or

(iii)a combination thereof;

wherein:

the CTC 11 gene is chromosomal, extra-chromosomal, or chromosomal and extra-chromosomal;

the CTC 09 gene, CTC 03 gene, or a combination thereof is chromosomal, extra-chromosomal, or a combination thereof;

expression of the CTC 11 gene is enhanced over that of a wild-type S. aureofaciens cell; and

optionally, the CTC 09 gene, the CTC 03 gene, or both of the CTC 09 gene and the CTC 03 gene are inactivated.

The present invention also contemplates vector pLP21329 and vectors for allelic replacement in a S. aureofaciens host cell. The vectors comprise:

(a) a functional E. coli origin of replication;

(b) a functional Streptomyces origin of replication;

(c) a functional gene that imparts a positively selectable phenotype on the host cell; and

((d) a ribosomal S12 gene which is expressed in Streptomyces such that it imparts sensitivity to streptomycin to the host cell.

In another embodiment, a method of mutating a target gene of a biosynthetic pathway of Streptomyces is disclosed. The method comprises

(a) replacing the genomic copy of the target gene with a selectable marker gene through homologous recombination to form a first recombinant strain; and

(b) replacing the selectable marker gene in the first recombinant strain with an altered copy of the target gene through homologous recombination to form a second recombinant strain.

12 Claims, 32 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 47

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw. Desc | Image

☐ 13. Document ID: US 5986080 A

L10: Entry 13 of 25 File: USPT Nov 16, 1999

US-PAT-NO: 5986080
DOCUMENT-IDENTIFIER: US 5986080 A

TITLE: Cloned nucleotide pyrophosphohydrolase and uses thereof

DATE-ISSUED: November 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Masuda; Ikuko	Wauwatosa	WI		
Barbieri; Joseph T.	New Berlin	WI		
Haas; Arthur L.	Brookfield	WI		
Halligan; Brian D.	Wauwatosa	WI		
McCarty; Daniel J.	Hartland	WI		
Ryan; Lawrence M.	Wauwatosa	WI		

US-CL-CURRENT: 536/23.2; 435/195, 435/252.3, 435/320.1, 530/350

ABSTRACT:

We have cloned and sequenced the cDNA encoding the 61 kD active fragment of a unique porcine chondrocyte nucleotide pyrophosphohydrolase (NTPPHase) from a porcine chondrocyte library. Degenerate oligonucleotides, corresponding to the N-terminal amino acid sequence of this peptide were hybridized to porcine chondrocyte cDNA and used to amplify DNA encoding the N-terminal sequence of 61 kD with the polymerase chain reaction (PCR). The PCR products were then used as probes to clone the entire open reading-frame for the 61 kD fragment from a porcine chondrocyte cDNA library. The length of the cloned cDNA was 2509 bp. Translation of the open-reading-frame predicts the 61 kD fragment to be a 459 amino acid protein. BLAST and FASTA analysis confirmed that this amino acid sequence was unique and did not possess high homology to any known proteins in the non-redundant protein data base. Limited homology (17%) between the 61 kD fragment and several prokaryotic and eukaryotic ATP pyrophosphate-lyase (adenylate cyclase) was detected. Northern blot analysis of porcine chondrocyte RNA showed that the DNA encoding the 61 kD fragment hybridized to a 4.3 kbp RNA transcript. Human chondrocyte RNA also hybridized to this porcine DNA probe. Coupled in vitro transcription translation of an expression vector containing the DNA insert in frame showed the expression of a 61 kD protein.

3 Claims, 9 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 9

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw Desc | Image

☐ 14. Document ID: US 5965429 A

L10: Entry 14 of 25 File: USPT Oct 12, 1999

US-PAT-NO: 5965429
DOCUMENT-IDENTIFIER: US 5965429 A

TITLE: Strain for the production of 6-demethyltetracycline, method for producing the strain and vector for use in the method

DATE-ISSUED: October 12, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ryan; Michael J.	West Milford	NJ		

US-CL-CURRENT: 435/252.35; 435/253.5, 435/320.1, 435/64, 435/889, 536/23.1

ABSTRACT:

Recombinant S. aureofaciens cells are provided. These cells comprise: (a) at least one CTC 11 gene; and (b) optionally

(i) a CTC 09 gene;

(ii) a CTC 03 gene; or

(iii) a combination thereof;

wherein:

the CTC 11 gene is chromosomal, extra-chromosomal, or chromosomal and extra-chromosomal;

the CTC 09 gene, CTC 03 gene, or a combination thereof is chromosomal, extra-chromosomal, or a combination thereof; expression of the CTC 11 gene is enhanced over that of a wild-type S. aureofaciens cell; and

optionally, the CTC 09 gene, the CTC 03 gene, or both of the CTC 09 gene and the CTC 03 gene are inactivated.

The present invention also contemplates vector pLP21329 and vectors for allelic replacement in a S. aureofaciens host cell. The vectors comprise:

(a) a functional E. coli origin of replication;

(b) a functional Streptomyces origin of replication;

(c) a functional gene that imparts a positively selectable phenotype on the host cell; and

((d) a ribosomal S12 gene which is expressed in Streptomyces such that it imparts sensitivity to streptomycin to the host cell. In another embodiment, a method of mutating a target gene of a biosynthetic pathway of Streptomyces is disclosed. The method comprises

(a) replacing the genomic copy of the target gene with a selectable marker gene through homologous recombination to form a first recombinant strain; and

(b) replacing the selectable marker gene in the first recombinant strain with an altered copy of the target gene through homologous recombination to form a second recombinant strain.

27 Claims, 48 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 47

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 15. Document ID: US 5955277 A

L10: Entry 15 of 25 File: USPT Sep 21, 1999

US-PAT-NO: 5955277
DOCUMENT-IDENTIFIER: US 5955277 A

TITLE: Mutant cDNA encoding the p85.alpha. subunit of phosphatidylinositol 3-kinase

DATE-ISSUED: September 21, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Hansen; Torben	Hellerup			DK
Andersen; Carsten Bo	Los Altos	CA		
Pedersen; Oluf Borbye	Holte			DK

US-CL-CURRENT: 435/6; 435/91.2, 536/23.1

ABSTRACT:

The present invention relates to a mutant cDNA sequence encoding the regulatory p85.alpha. subunit of phosphatidylinositol 3-kinase (PI3K), a method of detecting a mutation in the gene encoding the regulatory p85.alpha. subunit of phosphatidylinositol 3-kinase, as well as a diagnostic composition and a test kit for use in the method.

20 Claims, 2 Drawing figures
Exemplary Claim Number: 1

☐ 16. Document ID: US 5945292 A

L10: Entry 16 of 25 File: USPT Aug 31, 1999

US-PAT-NO: 5945292
DOCUMENT-IDENTIFIER: US 5945292 A

TITLE: Method of identifying cells with polypeptide surface marker

DATE-ISSUED: August 31, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Brizzard; Billy L.	New Haven	CT		
Bianca; Darlene W.	Westbrook	CT		
Chubet; Richard G.	Middletown	CT		
Vizard; Douglas L.	Cheshire	CT		
Hopp; Thomas Patrick	San Diego	CA		

US-CL-CURRENT: 435/7.21; 435/29, 435/34

ABSTRACT:

This invention discloses a gene for the identification of cells comprising a secretion leader segment, a cell marker segment and a transmembrane segment. The gene can be used to identify cells transfected with the gene by the steps of: inserting the gene having a secretion leader segment, a cell marker segment and a transmembrane segment into the DNA or RNA of a cell, allowing the cell to express the gene, and detecting the expressed cell marker segment of the gene.

10 Claims, 4 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 17. Document ID: US 5731425 A

L10: Entry 17 of 25 File: USPT Mar 24, 1998

US-PAT-NO: 5731425
DOCUMENT-IDENTIFIER: US 5731425 A

TITLE: Polypeptide surface marker for cells

DATE-ISSUED: March 24, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Brizzard; Billy L.	New Haven	CT		
Bianca; Darlene W.	Westbrook	CT		
Chubet; Richard G.	Middletown	CT		
Vizard; Douglas L.	Cheshire	CT		
Hopp; Thomas Patrick	San Diego	CA		

US-CL-CURRENT: 536/23.1; 435/320.1, 435/69.1, 536/24.1

ABSTRACT:

This invention discloses a gene for the identification of cells comprising a selection leader segment, a cell marker segment and a transmembrane segment. The gene can be used to identify cells transfected with the gene by the steps of: inserting the gene having a selection leader segment, a cell marker segment and a transmembrane segment into the DNA or RNA of a cell, allowing the cell to express the gene, and detecting the expressed cell marker segment of the gene.

12 Claims, 4 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 18. Document ID: US 5677153 A

L10: Entry 18 of 25 File: USPT Oct 14, 1997

US-PAT-NO: 5677153
DOCUMENT-IDENTIFIER: US 5677153 A

TITLE: Methods for modifying DNA and for detecting effects of such modification on interaction of encoded modified polypeptides with target substrates

DATE-ISSUED: October 14, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Botstein; David	Belmont	CA		
Palzkill; Timothy	Union City	CA		

US-CL-CURRENT: 435/91.4; 435/91.2, 435/91.41, 435/91.42

ABSTRACT:

The invention relates to methods and mutation linkers to modify DNA, to methods for producing libraries containing a multiplicity of modified DNA, and to methods for using such libraries for screening modified proteins encoded by such DNA. The DNA targeted for modification typically encodes a polypeptide such as an enzyme. The libraries are used to determine the effect of such modification or the interaction of the modified polypeptides with a target. In preferred embodiments, the invention relates to methods for making and using libraries containing DNA encoding modified antibiotic hydrolases to screen antibiotics against one or more of the modified antibiotic hydrolases produced by such libraries. Susceptibility or lack of susceptibility of an antibiotic to neutralization provides an indication of whether wild-type antibiotic hydrolases are likely to mutate to confer resistance to the antibiotic.

40 Claims, 55 Drawing figures
Exemplary Claim Number: 2
Number of Drawing Sheets: 23

☐ 19. Document ID: US 5670356 A

L10: Entry 19 of 25 File: USPT Sep 23, 1997

US-PAT-NO: 5670356
DOCUMENT-IDENTIFIER: US 5670356 A

TITLE: Modified luciferase

DATE-ISSUED: September 23, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Sherf; Bruce A.	Waunakee	WI		
Wood; Keith V.	Madison	WI		

US-CL-CURRENT: 435/189; 435/358, 435/364, 435/367, 435/394, 435/455, 536/23.2

ABSTRACT:

A modified form of beetle luciferase, which has been engineered for improved genetic reporting, is disclosed. The modified form contains one or more new features. Chief among these is removal of the peroxisomal translocation sequence to yield a cytoplasmic form of the enzyme. Other changes include removal of potentially interfering restriction sites and genetic regulatory sites from the gene, improvement of the codon usage for mammalian cells. The modified luciferase reporter enzyme is also devoid of potential N-glycosylation targets to minimize post-translational modification and remains in the cytoplasm of host cells to optimize substrate availability.

17 Claims, 6 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 6

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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20. Document ID: US 5650553 A

L10: Entry 20 of 25 File: USPT Jul 22, 1997

US-PAT-NO: 5650553
DOCUMENT-IDENTIFIER: US 5650553 A

TITLE: Plant genes for sensitivity to ethylene and pathogens

DATE-ISSUED: July 22, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ecker; Joseph	Erial	NJ		
Rothenberg; Madge	Haverford	PA		
Lehman; Anne	Philadelphia	PA		
Roman; Gregg	North Wales	PA		

US-CL-CURRENT: 800/298; 435/419, 514/12, 530/370, 536/23.6, 800/301

ABSTRACT:

The present invention is directed to nucleic acid sequences for ethylene insensitive, EIN loci and corresponding amino acid sequences. The present invention is also directed to nucleic acid sequences for hookless1, HLS1, alleles and amino acid sequences.

17 Claims, 42 Drawing figures
Exemplary Claim Number: 16
Number of Drawing Sheets: 35

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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Terms	Documents
common codon	25

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☐ 21. Document ID: US 5246844 A

L10: Entry 21 of 25 File: USPT Sep 21, 1993

US-PAT-NO: 5246844
DOCUMENT-IDENTIFIER: US 5246844 A

TITLE: Virulence associated proteins in Borrelia burgdorferi (BB)

DATE-ISSUED: September 21, 1993

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Norris; Steven J.	Houston	TX		
Barbour; Alan G.	San Antonio	TX		

US-CL-CURRENT: 435/480; 435/252.3, 435/252.33, 435/320.1, 435/476, 435/488, 536/23.7, 536/24.32, 536/24.33

ABSTRACT:

The invention relates to a DNA segment encoding a Borrelia burgdorferi antigenic polypeptide. The invention also relates to a purified 30 kDa polypeptide isolated from a virulent strain of B. burgdorferi and to epitopic segments of the polypeptide with immunogenic potential. The 30 kDa protein provides a route for the development of immunodiagnostics for Lyme disease and related disorders. The 30 kDa protein and related amino acid and DNA sequences may also be used for the immunization, for the detection of B. burgdorferi in human or animal tissues or body fluids, and also for the generation of specific antibodies for use in diagnosis, epidemiology, and prevention of Lyme disease.

22 Claims, 10 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 14

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

☐ 22. Document ID: US 5082767 A

L10: Entry 22 of 25 File: USPT Jan 21, 1992

US-PAT-NO: 5082767
DOCUMENT-IDENTIFIER: US 5082767 A

TITLE: Codon pair utilization

DATE-ISSUED: January 21, 1992

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Hatfield; G. Wesley	Corona Del Mar	CA	92625	
Gutman; George A.	Costa Mesa	CA	92626	

US-CL-CURRENT: 435/6; 435/69.1, 435/91.5, 436/501, 536/23.1, 536/24.1

ABSTRACT:

A method for determining the pattern of nonrandom codon pair usage of an organism, comprising the steps of obtaining nucleotide sequence data for the organism, determining from the data the number of codons represented in at least a portion of the sequence and the frequency of usage of at least some codons in the portion, determining from the frequency the expected number of occurrences of at least some codon pairs, if they are paired in a random manner, and comparing the expected number with the actual number of occurrences to determine relative codon pairing preferences. The codon pairings of organisms are highly nonrandom, and differ from organism to organism. This information is used to construct and express altered or synthetic genes having desired levels of translational efficiency, to determine which regions in a genome are protein coding regions, to introduce translational pause sites into heterologous genes, and to ascertain relationship or ancestral origin of nucleotide sequences.

44 Claims, 7 Drawing figures
Exemplary Claim Number: 1
Number of Drawing Sheets: 4

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 23. Document ID: WO 2064799 A2

L10: Entry 23 of 25 File: EPAB Aug 22, 2002

PUB-NO: WO002064799A2
DOCUMENT-IDENTIFIER: WO 2064799 A2
TITLE: OPTIMIZED MESSENGER RNA

PUBN-DATE: August 22, 2002

INVENTOR-INFORMATION:

NAME	COUNTRY
SELDON, RICHARD F	US
MILLER, ALLAN M	US
TRECO, DOUGLAS S	US

INT-CL (IPC): C12 N 15/67; C07 H 21/00; C07 K 14/745; C12 N 15/63
EUR-CL (EPC): C12N009/40; C07K014/745, C12N015/67

ABSTRACT:

The present invention is directed to a synthetic nucleic acid sequence which encodes a protein wherein at least one non-common codon or less-common codon is replaced by a common codon. The synthetic nucleic acid sequence can include a continuous stretch of at least 90 codons all of which are common codons.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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☐ 24. Document ID: AU 200177554 A DE 10037111 A1 WO 200210411 A2

L10: Entry 24 of 25 File: DWPI Feb 13, 2002

DERWENT-ACC-NO: 2002-189232
DERWENT-WEEK: 200238

TITLE: Preparing heterologous protein in prokaryotes, useful particularly for human growth hormone, with the coding sequence optimized for codon usage of the host

INVENTOR: BERGEMANN, K; GOETZ, F ; PESCHEL, A ; WERNER, R

PRIORITY-DATA: 2000DE-1037111 (July 27, 2000)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
AU 200177554 A	February 13, 2002		000	C12N015/67
DE 10037111 A1	February 7, 2002		016	C07H021/00
WO 200210411 A2	February 7, 2002	E	000	C12N015/67

INT-CL (IPC): C07 H 21/00; C12 N 1/21; C12 N 15/63; C12 N 15/67; C12 P 21/00; C12 P 21/08

ABSTRACTED-PUB-NO: DE 10037111A
BASIC-ABSTRACT:

NOVELTY - Preparation of a heterologous recombinant protein (I) in a prokaryotic host cell (A) in which:

(i) codon utilization of the host, for its own genes, is determined;

(ii) the nucleic acid (II) that encodes (I) is modified to replace rare codons (for the host) by common codons; and

(iii) cells are transformed with the modified sequence (IIa), for expression, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(a) similar method in which the host cell is transformed with nucleic acid encoding tRNA for rare codons;

(b) (IIa) in which at least one rare codon has been replaced by a common codon;

(c) a nucleic acid sequence (IIb) of about 1380 base pairs as given in the specification that encodes human growth hormone (hGH), also its fragments, sequences that hybridize to it under stringent conditions, its allelic or functional variants, and its variants within the degeneracy of the genetic code;

(d) vectors containing (IIa) or (IIb);

(e) host cells containing (IIa), (IIb) or the vectors of (d); and

(f) host cells containing one or more tRNA corresponding to codons rarely used by the cells.

USE - The method is used for production of antibodies, insulin, tissue plasminogen activator and particularly human growth hormone.

ADVANTAGE - Codon optimization and/or incorporation of tRNA for rare codons significantly increases expression rate of (I), and thus the yield, as less proteolysis occurs.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
Draw. Desc | Image

☐ 25. Document ID: AU 200178641 A WO 200204494 A2

L10: Entry 25 of 25 File: DWPI Jan 21, 2002

DERWENT-ACC-NO: 2002-171700
DERWENT-WEEK: 200234

TITLE: Selecting HIV-1 subtype C isolates, which are useful in developing vaccines against HIV infection, comprises isolating viruses with high sequence identity to a consensus sequence whose phenotype is associated with the HIV subtype

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PATENT-FAMILY:

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ABSTRACTED-PUB-NO: WO 200204494A
BASIC-ABSTRACT:

NOVELTY - Selecting human immunodeficiency virus (HIV) subtype isolates for use in the development of a prophylactic and/or therapeutic pharmaceutical composition, comprising selecting isolated virus or viruses with a high sequence identity to a consensus sequence, a phenotype which is associated with transmission for the particular HIV subtype, is new.

DETAILED DESCRIPTION - Selecting human immunodeficiency virus (HIV) subtype isolates for use in the development of a prophylactic and/or therapeutic pharmaceutical composition, comprising:

(a) isolating viruses from recently infected subjects;

(b) generating a consensus sequence for at least part of at least one HIV gene by identifying the most common codon or amino acid among the isolated viruses at each position along at least part of the gene; and

(c) selecting the isolated virus or viruses with a high sequence identity to the consensus sequence, a phenotype that is associated with transmission for the particular HIV subtype.

INDEPENDENT CLAIMS are also included for the following:

(1) HIV-1 subtype C isolates, which are designated Du422 (Provisional Accession Number 01032114, European Collection of Cell Cultures), Du151 (European Collection of Cell Cultures Accession Number 00072724) and Du179 (European Collection of Cell Cultures Accession Number 00072725);

(2) molecules comprising the nucleic acid sequences of the sequenced gag gene of the isolate Du422, pol gene of the isolate Du151 or env gene of the isolate Du151, where the sequences are not fully defined in the specification; or a 2579 base pair sequence, fully defined in the specification;

(3) polypeptides comprising the amino acid sequence of the sequenced gag gene of isolate Du422, pol gene of the isolate Du151 or env gene of the isolate Du151, where the sequences are not defined in the specification, an 858 residue amino acid sequence, fully defined in the specification, or a sequence that is a modification or derivative of them; and

(4) consensus amino acid sequence for the partial:

(a) gag gene of HIV-1 subtype C having a 313 residue amino acid sequence, fully defined in the specification;

(b) pol gene of HIV-1 subtype C having a 278 residue amino acid sequence, fully defined in the specification; or

(c) env gene of HlV-1 subtype C having a 229 residue amino acid sequence, fully defined in the specification.

ACTIVITY - Antiviral.

No biological data is given.

MECHANISM OF ACTION - Vaccine.

USE - For selecting HIV-1 subtype C isolates, which are useful in the development of a prophylactic and/or therapeutic pharmaceutical compositions, e.g. vaccines against HIV infection or disease.

Terms	Documents
common codon	25